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SEQUENCE LISTING

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CONEJO-GARCIA, Jose R

<120> IMMUNE CELL RECEPTOR LIGAND AND IMMUNE CELL RECEPTOR

<130> 555-88

<140> 10/525,643
<141> 2005-02-25

<150> PCT/US03/27488
<151> 2003-09-04

<150> 60/408,397
<151> 2002-09-04

<150> 60/478,371
<151> 2003-06-13

<160> 21

<170> PatentIn Ver. 2.1

<210> 1
<211> 148
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human ligand for NKG2D receptor

<400> 1
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atgcgaagaa tatccctgac ttctagccct gtgcgccttc ttttgtttct gctgttgcta 120
ctaatagcct tggagatcat ggttggtg 148

<210> 2
<211> 257
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human ligand for NKG2D receptor

<400> 2
gtcactctct ttgcttcaac ttcactataa aatcattgtc cagacctgga cagccctggt 60
gtgaagcgca ggtcttcttg aataaaaatc ttttccttca gtacaacagt gacaacaaca 120
tggtcaaacc tctgggcctc ctggggaaga aggtatatgc caccagcact tggggagaat 180
tgacccaaac gctgggagaa gtggggcgag acctcaggat gctcctttgt gacatcaaac 240
cccagataaa gaccagt 257

<210> 3
<211> 276
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human ligand for NKG2D receptor

<400> 3
gatccttcca ctctgcaagt cgagatgttt tgtcaacgtg aagcagaacg gtgcactggt 60
gcatcctggc agttcgccac caatggagag aaatccctcc tctttgacgc aatgaacatg 120
acctggacag taattaatca tgaagccagt aagatcaagg agacatggaa gaaagacaga 180
gggctggaaa agtatttcag gaagctctca aagggagact gcgatcactg gctcagggaa 240
ttcttagggc actgggaggc aatgccagaa ccgaca 276

<210> 4
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human ligand for NKG2D receptor

<400> 4
gtgtcaccag taaatgcttc agatatccac tggtcttctt ctagtctacc agatagatgg 60
atcatcctgg gggcattcat cctgttagtt ttaatgggaa ttgttctcat ctgtgtctgg 120
tggcaaaatg gtgagtggca ggctggtctc tggcccttga ggacgtctta gtctggtaag 180
gactcaagag aggtgaatca tggg 204

<210> 5
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ULBP1

<400> 5
Met Ala Ala Ala Ala Ser Pro Ala Phe Leu Leu Cys Leu Pro Leu Leu
1 5 10 15

His Leu Leu Ser Gly Trp Ser Arg Ala Gly Trp Val Asp Thr His Cys
20 25 30

Leu Cys Tyr Asp Phe Ile Ile Thr Pro Lys Ser Arg Pro Glu Pro Gln
35 40 45

Trp Cys Glu Val Gln Gly Leu Val Asp Glu Arg Pro Phe Leu His Tyr
50 55 60

Asp Cys Val Asn His Lys Ala Lys Ala Phe Ala Ser Leu Gly Lys Lys
65 70 75 80

Val Asn Val Thr Lys Thr Trp Glu Glu Gln Thr Glu Thr Leu Arg Asp

```
                85                  90                  95

Val Val Asp Phe Leu Lys Gly Gln Leu Leu Asp Ile Gln Val Glu Asn
            100                 105                 110

Leu Ile Pro Ile Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
        115                 120                 125

His Glu Ala His Gly His Gly Arg Gly Ser Trp Gln Phe Leu Phe Asn
    130                 135                 140

Gly Gln Lys Phe Leu Leu Phe Asp Ser Asn Asn Arg Lys Trp Thr Ala
145                 150                 155                 160

Leu His Pro Gly Ala Lys Lys Met Thr Glu Lys Trp Glu Lys Asn Arg
                165                 170                 175

Asp Val Thr Met Phe Phe Gln Lys Ile Ser Leu Gly Asp Cys Lys Met
            180                 185                 190

Trp Leu Glu Glu Phe Leu Met Tyr Trp Glu Gln Met Leu Asp Pro Thr
        195                 200                 205

Lys Pro Pro Ser Leu Ala Pro Gly Thr Thr Gln Pro Lys Ala Met Ala
    210                 215                 220

Thr Thr Leu Ser Pro Trp Ser Leu Leu Ile Ile Phe Leu Cys Phe Ile
225                 230                 235                 240

Leu Ala Gly Arg
```

<210> 6
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ULBP2

<400> 6

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Met Ala Ala Ala Ala Ala Thr Lys Ile Leu Leu Cys Leu Pro Leu Leu
  1               5                  10                  15

Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro His Ser
             20                  25                  30

Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
         35                  40                  45

Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
     50                  55                  60

Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
 65                  70                  75                  80
```

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Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
                 85                  90                  95

Val Val Asp Ile Leu Thr Glu Gln Leu Arg Asp Ile Gln Leu Glu Asn
            100                 105                 110

Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu

        115                 120                 125

Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln Phe Ser Phe Asp
    130                 135                 140

Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Lys Arg Met Trp Thr Thr
145                 150                 155                 160

Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
                165                 170                 175

Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly
            180                 185                 190

Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
        195                 200                 205

Ala Gly Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala
    210                 215                 220

Thr Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys
225                 230                 235                 240

Phe Ile Leu Pro Gly Ile
                245
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<210> 7
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ULBP3

<400> 7

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Met Ala Ala Ala Ala Ser Pro Ala Ile Leu Pro Arg Leu Ala Ile Leu
  1               5                  10                  15

Pro Tyr Leu Leu Phe Asp Trp Ser Gly Thr Gly Arg Ala Asp Ala His
             20                  25                  30

Ser Leu Trp Tyr Asn Phe Thr Ile Ile His Leu Pro Arg His Gly Gln
         35                  40                  45

Gln Trp Cys Glu Val Gln Ser Gln Val Asp Gln Lys Asn Phe Leu Ser
     50                  55                  60

Tyr Asp Cys Gly Ser Asp Lys Val Leu Ser Met Gly His Leu Glu Glu
```

```
 65                  70                  75                  80

Gln Leu Tyr Ala Thr Asp Ala Trp Gly Lys Gln Leu Glu Met Leu Arg
                 85                  90                  95

Glu Val Gly Gln Arg Leu Arg Leu Glu Leu Ala Asp Thr Glu Leu Glu
            100                 105                 110

Asp Phe Thr Pro Ser Gly Pro Leu Thr Leu Gln Val Arg Met Ser Cys
        115                 120                 125

Glu Cys Glu Ala Asp Gly Tyr Ile Arg Gly Ser Trp Gln Phe Ser Phe
    130                 135                 140

Asp Gly Arg Lys Phe Leu Leu Phe Asp Ser Asn Asn Arg Lys Trp Thr
145                 150                 155                 160

Val Val His Ala Gly Ala Arg Arg Met Lys Glu Lys Trp Glu Lys Asp
                165                 170                 175

Ser Gly Leu Thr Thr Phe Phe Lys Met Val Ser Met Arg Asp Cys Lys
            180                 185                 190

Ser Trp Leu Arg Asp Phe Leu Met His Arg Lys Lys Arg Leu Glu Pro
        195                 200                 205

Thr Ala Pro Pro Thr Met Ala Pro Gly Leu Ala Gln Pro Lys Ala Ile
    210                 215                 220

Ala Thr Thr Leu Ser Pro Trp Ser Phe Leu Ile Ile Leu Cys Phe Ile
225                 230                 235                 240

Leu Pro Gly Ile
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<210> 8
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human ligand for NKG2D receptor

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<400> 8
Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Phe
  1               5                  10                  15

Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
             20                  25                  30

Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
         35                  40                  45

Trp Cys Glu Ala Gln Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
     50                  55                  60
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```
Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
 65                  70                  75                  80

Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
                 85                  90                  95

Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile
            100                 105                 110

Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Glu Met Phe Cys Gln Arg
        115                 120                 125

Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly
    130                 135                 140

Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile
145                 150                 155                 160

Asn His Glu Ala Ser Lys Ile Lys Glu Thr Trp Lys Lys Asp Arg Gly
                165                 170                 175

Leu Glu Lys Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp
            180                 185                 190

Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Glu Pro Thr Val
        195                 200                 205

Ser Pro Val Asn Ala Ser Asp Ile His Trp Ser Ser Ser Ser Leu Pro
    210                 215                 220

Asp Arg Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Val Leu Met Gly
225                 230                 235                 240

Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Glu Trp Gln Ala Gly
                245                 250                 255

Leu Trp Pro Leu Arg Thr Ser
            260
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<210> 9
<211> 710
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cDNA sequence of immune cell receptor LCCR

<400> 9
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tttcgagcac atgtgttttt atgagaatta tgctgagata gatttcttta catattcatc 60
aatgtctgaa gaagttactt atgcagatct tcaattccag aactccagtg agatggaaaa 120
aatcccagaa attggcaaat ttggggaaaa agcacctcca gctcccctctc atgtatggcg 180
tccagcagcc ttgtttctga ctcttctgtg ccttctgttg ctcattggat tgggagtctt 240
ggcaagcatg tttcacgtaa ctttgaagat agaaatgaaa aaaatgaaca aactacaaaa 300
catcagtgaa gagctccaga gaaatatttc tctacaactg atgagtaaca tgaatatctc 360
caacaagatc aggaacctct ccaccacact gcaaacaata gccaccaaat tatgtcgtga 420
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gctatatagc aaagaacaag agcacaaatg taagccttgt ccaaggagat ggatttggca 480
taaggacagc tgttatttcc taagtgatga tgtccaaaca tggcaggaga gtaaaatggc 540
ctgtgctgct cagaatgcca gcctgttgaa gataaacaac aaaaatgcat tggaatttat 600
aaaatcccag agtagatcat atgactattg gctgggatta tctcctgaag aagattccac 660
tcgtggtatg agagtggata atataatcaa ctcctctgcc tggtaagtgt 710

<210> 10
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Immune LCCR cell receptor

<400> 10
Met Cys Phe Tyr Glu Asn Tyr Ala Glu Ile Asp Phe Phe Thr Tyr Ser
1 5 10 15

Ser Met Ser Glu Glu Val Thr Tyr Ala Asp Leu Gln Phe Gln Asn Ser
20 25 30

Ser Glu Met Glu Lys Ile Pro Glu Ile Gly Lys Phe Gly Glu Lys Ala
35 40 45

Pro Pro Ala Pro Ser His Val Trp Arg Pro Ala Ala Leu Phe Leu Thr
50 55 60

Leu Leu Cys Leu Leu Leu Leu Ile Gly Leu Gly Val Leu Ala Ser Met
65 70 75 80

Phe His Val Thr Leu Lys Ile Glu Met Lys Lys Met Asn Lys Leu Gln
85 90 95

Asn Ile Ser Glu Glu Leu Gln Arg Asn Ile Ser Leu Gln Leu Met Ser
100 105 110

Asn Met Asn Ile Ser Asn Lys Ile Arg Asn Leu Ser Thr Thr Leu Gln
115 120 125

Thr Ile Ala Thr Lys Leu Cys Arg Glu Leu Tyr Ser Lys Glu Gln Glu
130 135 140

His Lys Cys Lys Pro Cys Pro Arg Arg Trp Ile Trp His Lys Asp Ser
145 150 155 160

Cys Tyr Phe Leu Ser Asp Asp Val Gln Thr Trp Gln Glu Ser Lys Met
165 170 175

Ala Cys Ala Ala Gln Asn Ala Ser Leu Leu Lys Ile Asn Asn Lys Asn
180 185 190

Ala Leu Glu Phe Ile Lys Ser Gln Ser Arg Ser Tyr Asp Tyr Trp Leu
195 200 205

Gly Leu Ser Pro Glu Glu Asp Ser Thr Arg Gly Met Arg Val Asp Asn
210 215 220

Ile Ile Asn Ser Ser Ala Trp
225 230

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 11
ccataccagt gagggtgaat g 21

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 12
cccatgattc acctctcttg ag 22

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 13
ctcaggatgc tcctttgtga cat 23

<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 14
cttcacgttg acaaaacatc tcg 23

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 15
cccagataaa gaccagtgat ccttccact 29

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 16
cctgcaccac caactgctta 20

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 17
catgagtcct tccacgatac ca 22

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 18
cctggccaag gtcatccatg acaac 25

<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 19
gcaatgatgt actgtctctt ttgga 25

<210> 20

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 20
caacctcagc caagtaacgg tag 23

<210> 21
<211> 885
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human ligand for NKG2D receptor

<400> 21
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atgcgaagaa tatccctgac ttctagccct gtgcgccttc ttttgtttct gctgttgcta 120
ctaatagcct tggagatcat ggttggtggt cactctcttt gcttcaactt cactataaaa 180
tcattgtcca gacctggaca gccctggtgt gaagcgcagg tcttcttgaa taaaaatctt 240
ttccttcagt acaacagtga caacaacatg gtcaaacctc tgggcctcct ggggaagaag 300
gtatatgcca ccagcacttg gggagaattg acccaaacgc tgggagaagt ggggcgagac 360
ctcaggatgc tcctttgtga catcaaaccc cagataaaga ccagtgatcc ttccactctg 420
caagtcgaga tgttttgtca acgtgaagca gaacggtgca ctggtgcatc ctggcagttc 480
gccaccaatg gagagaaatc cctcctcttt gacgcaatga acatgacctg gacagtaatt 540
aatcatgaag ccagtaagat caaggagaca tggaagaaag acagagggct ggaaaagtat 600
ttcaggaagc tctcaaaggg agactgcgat cactggctca gggaattctt agggcactgg 660
gaggcaatgc cagaaccgac agtgtcacca gtaaatgctt cagatatcca ctggtcttct 720
tctagtctac cagatagatg gatcatcctg ggggcattca tcctgttagt tttaatggga 780
attgttctca tctgtgtctg gtggcaaaat ggtgagtggc aggctggtct ctggcccttg 840
aggacgtctt agtctggtaa ggactcaaga gaggtgaatc atggg 885